0186

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/211,785

CRF Processing Date: 12/23/98
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

_____

ENTERED

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☑ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: 35

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: seq 18 - inserted generic parentheses

_____

_____

_____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Jones, Kenneth A.
Laz, Thomas M.
Borowsky, Beth

(ii) TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And Uses Thereof

--> **(iii) NUMBER OF SEQUENCES: 47**

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
--> **(A) APPLICATION NUMBER: Not Yet Known**
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White Esq., John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 54002-D

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-278-0400
(B) TELEFAX: 212-391-0525

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCATGCCGCT CACCAAGGAG GTGGCC 26

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

--> **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:**

GGCCACCTCC TTGGTGAGCG GCATGA 26

--> **(2) INFORMATION FOR SEQ ID NO:19:**

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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 948      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
 949
 950  TGAGTGAGCA GAGTCCAGAG CCGT                                        24
 951
 952
```

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1244  (2) INFORMATION FOR SEQ ID NO:35:
1245
1246       (i) SEQUENCE CHARACTERISTICS:
--> 1247        (A) LENGTH: 29 base pairs
1248            (B) TYPE: nucleic acid
1249            (C) STRANDEDNESS: single
1250            (D) TOPOLOGY: linear
1251
1252      (ii) MOLECULE TYPE: other nucleic acid
1253
1254     (iii) HYPOTHETICAL: NO
1255
1256      (iv) ANTI-SENSE: NO
1257
1258      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
1259
1260  CCGGAATTCC CCTCACACCG AGCCCCTGG                                    29 Correct
1261
1262
```

```
1597  (2) INFORMATION FOR SEQ ID NO:47:
1598
1599       (i) SEQUENCE CHARACTERISTICS:
1600            (A) LENGTH: 941 amino acids
1601            (B) TYPE: amino acid
1602            (C) STRANDEDNESS: single
1603            (D) TOPOLOGY: Not Relevant
1604
1605      (ii) MOLECULE TYPE: protein
1606
1607     (iii) HYPOTHETICAL: NO
1608
1609
1610
1611
1612      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
1613
1614       Met Ala Ser Pro Arg Ser Ser Gly Gln Pro Gly Pro Pro Pro Pro Pro
1615       1               5                  10                  15
1616
1617       Pro Pro Pro Pro Ala Arg Leu Leu Leu Leu Leu Leu Leu Pro Leu Leu
1618                   20                  25                  30
1619
1620       Leu Pro Leu Ala Pro Gly Ala Trp Gly Trp Ala Arg Gly Ala Pro Arg
1621               35                  40                  45
1622
1623       Pro Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu
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1624          50                  55                  60
1625
1626      Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala
1627      65                  70                  75                  80
1628
1629      Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro
1630                      85                  90                  95
1631
1632      Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys
1633                  100                 105                 110
1634
1635      Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr Gly Pro Asn His Leu
1636              115                 120                 125
1637
1638      Met Val Phe Gly Gly Val Cys Pro Ser Val Thr Ser Ile Ile Ala Glu
1639          130                 135                 140
1640
1641      Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser Phe Ala Ala Thr Thr
1642      145                 150                 155                 160
1643
1644      Pro Val Leu Ala Asp Lys Lys Lys Tyr Pro Tyr Phe Phe Arg Thr Val
1645                      165                 170                 175
1646
1647      Pro Ser Asp Asn Ala Val Asn Pro Ala Ile Leu Lys Leu Leu Lys His
1648                  180                 185                 190
1649
1650      Tyr Gln Trp Lys Arg Val Gly Thr Leu Thr Gln Asp Val Gln Arg Phe
1651              195                 200                 205
1652
1653      Ser Glu Val Arg Asn Asp Leu Thr Gly Val Leu Tyr Gly Glu Asp Ile
1654          210                 215                 220
1655
1656      Glu Ile Ser Asp Thr Glu Ser Phe Ser Asn Asp Pro Cys Thr Ser Val
1657      225                 230                 235                 240
1658
1659      Lys Lys Leu Lys Gly Asn Asp Val Arg Ile Ile Leu Gly Gln Phe Asp
1660                      245                 250                 255
1661
1662      Gln Asn Met Ala Ala Lys Val Phe Cys Cys Ala Tyr Glu Glu Asn Met
1663                  260                 265                 270
1664
1665      Tyr Gly Ser Lys Tyr Gln Trp Ile Ile Pro Gly Trp Tyr Glu Pro Ser
1666              275                 280                 285
1667
1668      Trp Trp Glu Gln Val His Thr Glu Ala Asn Ser Ser Arg Cys Leu Arg
1669          290                 295                 300
1670
1671      Lys Asn Leu Leu Ala Ala Met Glu Gly Tyr Ile Gly Val Asp Phe Glu
1672      305                 310                 315                 320
1673
1674      Pro Leu Ser Ser Lys Gln Ile Lys Thr Ile Ser Gly Lys Thr Pro Gln
1675                      325                 330                 335
1676
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1677        Gln Tyr Glu Arg Glu Tyr Asn Asn Lys Arg Ser Gly Val Gly Pro Ser
1678                    340                 345                 350
1679
1680        Lys Phe His Gly Tyr Ala Tyr Asp Gly Ile Trp Val Ile Ala Lys Thr
1681                355                 360                 365
1682
1683        Leu Gln Arg Ala Met Glu Thr Leu His Ala Ser Ser Arg His Gln Arg
1684            370                 375                 380
1685
1686        Ile Gln Asp Phe Asn Tyr Thr Asp His Thr Leu Gly Arg Ile Ile Leu
1687        385                 390                 395                 400
1688
1689        Asn Ala Met Asn Glu Thr Asn Phe Phe Gly Val Thr Gly Gln Val Val
1690                        405                 410                 415
1691
1692        Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys Phe Thr Gln Phe Gln
1693                    420                 425                 430
1694
1695        Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn Ala Val Ala Asp Thr
1696                435                 440                 445
1697
1698        Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln Gly Ser Glu Pro Pro
1699            450                 455                 460
1700
1701        Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg Lys Ile Ser Leu Pro
1702        465                 470                 475                 480
1703
1704        Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu Gly Met Ile Met Ala
1705                        485                 490                 495
1706
1707        Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg Asn Gln Lys Leu Ile
1708                    500                 505                 510
1709
1710        Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile Ile Leu Gly Gly Met
1711                515                 520                 525
1712
1713        Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu Asp Gly Ser Phe Val
1714            530                 535                 540
1715
1716        Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val Arg Thr Trp Ile Leu
1717        545                 550                 555                 560
1718
1719        Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met Phe Ala Lys Thr Trp
1720                        565                 570                 575
1721
1722        Arg Val His Ala Ile Phe Lys Asn Val Lys Met Lys Lys Lys Ile Ile
1723                    580                 585                 590
1724
1725        Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly Met Leu Leu Ile Asp
1726                595                 600                 605
1727
1728        Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp Pro Leu Arg Arg Thr
1729            610                 615                 620
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1730
1731  Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala Gly Arg Asp Ile Ser
1732  625                 630                 635                 640
1733
1734  Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr His Met Thr Ile Trp
1735                      645                 650                 655
1736
1737  Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu Met Leu Phe Gly Cys
1738              660                 665                 670
1739
1740  Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile Pro Ala Leu Asn Asp
1741          675                 680                 685
1742
1743  Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val Gly Ile Met Cys Ile
1744      690                 695                 700
1745
1746  Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp Gln Pro Asn Val Gln
1747  705                 710                 715                 720
1748
1749  Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys Ser Thr Ile Thr Leu
1750                      725                 730                 735
1751
1752  Cys Leu Val Phe Val Pro Lys Leu Ile Thr Leu Arg Thr Asn Pro Asp
1753              740                 745                 750
1754
1755  Ala Ala Thr Gln Asn Arg Arg Phe Gln Phe Thr Gln Asn Gln Lys Lys
1756          755                 760                 765
1757
1758  Glu Asp Ser Lys Thr Ser Thr Ser Val Thr Ser Val Asn Gln Ala Ser
1759      770                 775                 780
1760
1761  Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn His Arg Leu Arg Met
1762  785                 790                 795                 800
1763
1764  Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu Val Thr Met Gln Leu
1765                      805                 810                 815
1766
1767  Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys Gln Asn His Tyr Gln
1768              820                 825                 830
1769
1770  Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe Thr Glu Ser Thr Asp
1771          835                 840                 845
1772
1773  Gly Gly Lys Ala Ile Leu Lys Asn His Leu Asp Gln Asn Pro Gln Leu
1774      850                 855                 860
1775
1776  Gln Trp Asn Thr Thr Glu Pro Ser Arg Thr Cys Lys Asp Pro Ile Glu
1777  865                 870                 875                 880
1778
1779  Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg Leu Ser Leu Gln Leu
1780                      885                 890                 895
1781
1782  Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile Gly Gly Val Asp Ala
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1783                  900                 905                 910
1784
1785       Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala Ser Pro Arg His Arg
1786               915                 920                 925
1787
1788       His Val Pro Pro Ser Phe Arg Val Met Val Ser Gly Leu
1789           930                 935                 940
1790
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/211,755*

DATE: 12/23/98
TIME: 14:07:31

INPUT SET: S30470.raw

Line	Error	Original Text
12	Number of Sequences (47) Doesn't Equal Actual Count (46)	(iii) NUMBER OF SEQUENCES: 47
29	Wrong application Serial Number	(A) APPLICATION NUMBER: Not Yet Known
929	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
934	Sequence 18 missing	(2) INFORMATION FOR SEQ ID NO:19:
1247	Entered (29) and Calc. Seq. Length (0) differ	(A) LENGTH: 29 base pairs